

SEQUENCE LISTING

<110> GARGER, Stephen A.
TURPEN, Thomas H.
KUMAGAI, Monto H.

<120> PRODUCTION OF LYSOSOMAL ENZYMES IN
PLANTS BY TRANSIENT EXPRESSION

<130> 008010087CPUS06

<140> To Be Assigned

<141> 2001-11-13

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<212> PRT

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87

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Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser			
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Phe	Pro	His	Gly	Ile	Arg	Gln	Leu	Ala	Asn	Tyr	Val	His	Ser	Lys	Gly
		115				120						125			
Leu	Lys	Leu	Gly	Ile	Tyr	Ala	Asp	Val	Gly	Asn	Lys	Thr	Cys	Ala	Gly
		130				135					140				
Phe	Pro	Gly	Ser	Phe	Gly	Tyr	Tyr	Asp	Ile	Asp	Ala	Gln	Thr	Phe	Ala
145					150					155					160
Asp	Trp	Gly	Val	Asp	Leu	Leu	Lys	Phe	Asp	Gly	Cys	Tyr	Cys	Asp	Ser
				165					170					175	
Leu	Glu	Asn	Leu	Ala	Asp	Gly	Tyr	Lys	His	Met	Ser	Leu	Ala	Leu	Asn
		180						185					190		
Arg	Thr	Gly	Arg	Ser	Ile	Val	Tyr	Ser	Cys	Glu	Trp	Pro	Leu	Tyr	Met
		195				200						205			
Trp	Pro	Phe	Gln	Lys	Pro	Asn	Tyr	Thr	Glu	Ile	Arg	Gln	Tyr	Cys	Asn
	210					215					220				
His	Trp	Arg	Asn	Phe	Ala	Asp	Ile	Asp	Asp	Ser	Trp	Lys	Ser	Ile	Lys
225					230					235					240
Ser	Ile	Leu	Asp	Trp	Thr	Ser	Phe	Asn	Gln	Glu	Arg	Ile	Val	Asp	Val
				245					250					255	
Ala	Gly	Pro	Gly	Gly	Trp	Asn	Asp	Pro	Asp	Met	Leu	Val	Ile	Gly	Asn
			260					265					270		
Phe	Gly	Leu	Ser	Trp	Asn	Gln	Gln	Val	Thr	Gln	Met	Ala	Leu	Trp	Ala
		275					280					285			
Ile	Met	Ala	Ala	Pro	Leu	Phe	Met	Ser	Asn	Asp	Leu	Arg	His	Ile	Ser
	290					295					300				
Pro	Gln	Ala	Lys	Ala	Leu	Leu	Gln	Asp	Lys	Asp	Val	Ile	Ala	Ile	Asn
305					310					315					320
Gln	Asp	Pro	Leu	Gly	Lys	Gln	Gly	Tyr	Gln	Leu	Arg	Gln	Gly	Asp	Asn
				325					330					335	
Phe	Glu	Val	Trp	Glu	Arg	Pro	Leu	Ser	Gly	Leu	Ala	Trp	Ala	Val	Ala
		340						345					350		
Met	Ile	Asn	Arg	Gln	Glu	Ile	Gly	Pro	Arg	Ser	Tyr	Thr	Ile	Ala	
	355					360					365				
Val	Ala	Ser	Leu	Gly	Lys	Gly	Val	Ala	Cys	Asn	Pro	Ala	Cys	Phe	Ile

370		375		380
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr				
385		390		395
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln				400
	405		410	415
Leu Glu Asn Thr Met Gln Met Ser Leu Ser Glu Lys Asp Glu Leu				
420		425		430

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1266)

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Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu	
1 5 10 15	
cgc ttc ctg gcc ctc gtt tcc tgg gac atc cct ggg gct aga gca ctg	96
Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu	
20 25 30	
gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag	144
Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu	
35 40 45	
cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc	192
Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile	
50 55 60	
agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc	240
Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly	
65 70 75 80	
tgg aag gat gca ggt tat gag tac ctc tgc att gat gac tgt tgg atg	288
Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met	
85 90 95	
gct ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag cgc	336
Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg	
100 105 110	
ttt cct cat ggg att cgc cag cta gct aat tat gtt cac agc aaa gga	384
Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly	
115 120 125	
ctg aag cta ggg att tat gca gat gtt gga aat aaa acc tgc gca ggc	432
Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly	
130 135 140	

ttc cct ggg agt ttt gga tac tac gac att gat gcc cag acc ttt gct	480
Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala	
145 150 155 160	
gac tgg gga gta gat ctg cta aaa ttt gat ggt tgt tac tgt gac agt	528
Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser	
165 170 175	
ttg gaa aat ttg gca gat ggt tat aag cac atg tcc ttg gcc ctg aat	576
Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn	
180 185 190	
agg act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg	624
Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met	
195 200 205	
tgg ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat	672
Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn	
210 215 220	
cac tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag	720
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys	
225 230 235 240	
agt atc ttg gac tgg aca tct ttt aac cag gag aga att gtt gat gtt	768
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val	
245 250 255	
gct gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac	816
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn	
260 265 270	
ttt ggc ctc agc tgg aat cag caa gta act cag atg gcc ctc tgg gct	864
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala	
275 280 285	
atc atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc	912
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser	
290 295 300	
cct caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat	960
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn	
305 310 315 320	
cag gac ccc ttg ggc aag caa ggg tac cag ctt aga cag gga gac aac	1008
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn	
325 330 335	
ttt gaa gtg tgg gaa cga cct ctc tca ggc tta gcc tgg gct gta gct	1056
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala	
340 345 350	
atg ata aac cgg cag gag att ggt gga cct cgc tct tat acc atc gca	1104
Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala	

355	360	365	
gtt gct tcc ctg ggt aaa gga gtg gcc tgt aat cct gcc tgc ttc atc			1152
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile			
370	375	380	
aca cag ctc ctc cct gtg aaa agg aag cta ggg ttc tat gaa tgg act			1200
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr			
385	390	395	400
tca agg tta aga agt cac ata aat ccc aca ggc act gtt ttg ctt cag			1248
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln			
405	410	415	
cta gaa aac aca atg taa			1266
Leu Glu Asn Thr Met *			
420			

<210> 12
 <211> 421
 <212> PRT
 <213> Homo sapiens

<400> 12

Met	Gln	Leu	Arg	Asn	Pro	Glu	Leu	His	Leu	Gly	Cys	Ala	Leu	Ala	Leu
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Arg	Phe	Leu	Ala	Leu	Val	Ser	Trp	Asp	Ile	Pro	Gly	Ala	Arg	Ala	Leu
			20					25					30		
Asp	Asn	Gly	Leu	Ala	Arg	Thr	Pro	Thr	Met	Gly	Trp	Leu	His	Trp	Glu
		35				40						45			
Arg	Phe	Met	Cys	Asn	Leu	Asp	Cys	Gln	Glu	Glu	Pro	Asp	Ser	Cys	Ile
	50				55					60					
Ser	Glu	Lys	Leu	Phe	Met	Glu	Met	Ala	Glu	Leu	Met	Val	Ser	Glu	Gly
65				70						75					80
Trp	Lys	Asp	Ala	Gly	Tyr	Glu	Tyr	Leu	Cys	Ile	Asp	Asp	Cys	Trp	Met
			85					90						95	
Ala	Pro	Gln	Arg	Asp	Ser	Glu	Gly	Arg	Leu	Gln	Ala	Asp	Pro	Gln	Arg
			100					105					110		
Phe	Pro	His	Gly	Ile	Arg	Gln	Leu	Ala	Asn	Tyr	Val	His	Ser	Lys	Gly
			115				120					125			
Leu	Lys	Leu	Gly	Ile	Tyr	Ala	Asp	Val	Gly	Asn	Lys	Thr	Cys	Ala	Gly
	130					135					140				
Phe	Pro	Gly	Ser	Phe	Gly	Tyr	Tyr	Asp	Ile	Asp	Ala	Gln	Thr	Phe	Ala
145				150						155					160
Asp	Trp	Gly	Val	Asp	Leu	Leu	Lys	Phe	Asp	Gly	Cys	Tyr	Cys	Asp	Ser
			165					170						175	
Leu	Glu	Asn	Leu	Ala	Asp	Gly	Tyr	Lys	His	Met	Ser	Leu	Ala	Leu	Asn
		180					185						190		
Arg	Thr	Gly	Arg	Ser	Ile	Val	Tyr	Ser	Cys	Glu	Trp	Pro	Leu	Tyr	Met
	195					200						205			
Trp	Pro	Phe	Gln	Lys	Pro	Asn	Tyr	Thr	Glu	Ile	Arg	Gln	Tyr	Cys	Asn
	210				215						220				
His	Trp	Arg	Asn	Phe	Ala	Asp	Ile	Asp	Asp	Ser	Trp	Lys	Ser	Ile	Lys

225					230					235					240
Ser	Ile	Leu	Asp	Trp	Thr	Ser	Phe	Asn	Gln	Glu	Arg	Ile	Val	Asp	Val
				245					250					255	
Ala	Gly	Pro	Gly	Gly	Trp	Asn	Asp	Pro	Asp	Met	Leu	Val	Ile	Gly	Asn
			260					265					270		
Phe	Gly	Leu	Ser	Trp	Asn	Gln	Gln	Val	Thr	Gln	Met	Ala	Leu	Trp	Ala
		275					280					285			
Ile	Met	Ala	Ala	Pro	Leu	Phe	Met	Ser	Asn	Asp	Leu	Arg	His	Ile	Ser
	290					295				300					
Pro	Gln	Ala	Lys	Ala	Leu	Leu	Gln	Asp	Lys	Asp	Val	Ile	Ala	Ile	Asn
305					310				315					320	
Gln	Asp	Pro	Leu	Gly	Lys	Gln	Gly	Tyr	Gln	Leu	Arg	Gln	Gly	Asp	Asn
			325					330					335		
Phe	Glu	Val	Trp	Glu	Arg	Pro	Leu	Ser	Gly	Leu	Ala	Trp	Ala	Val	Ala
		340					345					350			
Met	Ile	Asn	Arg	Gln	Glu	Ile	Gly	Gly	Pro	Arg	Ser	Tyr	Thr	Ile	Ala
	355					360				365					
Val	Ala	Ser	Leu	Gly	Lys	Gly	Val	Ala	Cys	Asn	Pro	Ala	Cys	Phe	Ile
	370				375					380					
Thr	Gln	Leu	Leu	Pro	Val	Lys	Arg	Lys	Leu	Gly	Phe	Tyr	Glu	Trp	Thr
385				390					395					400	
Ser	Arg	Leu	Arg	Ser	His	Ile	Asn	Pro	Thr	Gly	Thr	Val	Leu	Leu	Gln
			405					410					415		
Leu	Glu	Asn	Thr	Met											
			420												

<210> 13
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1284)

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1 5 10 15	
cgc ttc ctg gcc ctc gtt tcc tgg gac atc cct ggg gct aga gca ctg	96
Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu	
20 25 30	
gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag	144
Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu	
35 40 45	
cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc	192
Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile	
50 55 60	
agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc	240
Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly	

65	70	75	80	
tgg aag gat gca ggt tat gag tac ctc tgc att gat gac tgt tgg atg				288
Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met	85	90	95	
gct ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag cgc				336
Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg	100	105	110	
ttt cct cat ggg att cgc cag cta gct aat tat gtt cac agc aaa gga				384
Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly	115	120	125	
ctg aag cta ggg att tat gca gat gtt gga aat aaa acc tgc gca ggc				432
Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly	130	135	140	
ttc cct ggg agt ttt gga tac tac gac att gat gcc cag acc ttt gct				480
Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala	145	150	155	160
gac tgg gga gta gat ctg cta aaa ttt gat ggt tgt tac tgt gac agt				528
Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser	165	170	175	
ttg gaa aat ttg gca gat ggt tat aag cac atg tcc ttg gcc ctg aat				576
Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn	180	185	190	
agg act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg				624
Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met	195	200	205	
tgg ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat				672
Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn	210	215	220	
cac tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag				720
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys	225	230	235	240
agt atc ttg gac tgg aca tct ttt aac cag gag aga att gtt gat gtt				768
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val	245	250	255	
gct gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac				816
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn	260	265	270	
ttt ggc ctc agc tgg aat cag caa gta act cag atg gcc ctc tgg gct				864
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala	275	280	285	

atg cag ctg agg aac cca gaa cta cat ctg ggc tgc gcg ctt gcg ctt	48
Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu	
1 5 10 15	
cgc ttc ctg gcc ctc gtt tcc tgg gac atc cct ggg gct aga gca ctg	96
Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu	
20 25 30	
gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag	144
Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu	
35 40 45	
cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc	192
Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile	
50 55 60	
agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc	240
Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly	
65 70 75 80	
tgg aag gat gca ggt tat gag tac ctc tgc att gat gac tgt tgg atg	288
Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met	
85 90 95	
gct ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag cgc	336
Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg	
100 105 110	
ttt cct cat ggg att cgc cag cta gct aat tat gtt cac agc aaa gga	384
Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly	
115 120 125	
ctg aag cta ggg att tat gca gat gtt gga aat aaa acc tgc gca ggc	432
Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly	
130 135 140	
ttc cct ggg agt ttt gga tac tac gac att gat gcc cag acc ttt gct	480
Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala	
145 150 155 160	
gac tgg gga gta gat ctg cta aaa ttt gat ggt tgt tac tgt gac agt	528
Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser	
165 170 175	
ttg gaa aat ttg gca gat ggt tat aag cac atg tcc ttg gcc ctg aat	576
Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn	
180 185 190	
agg act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg	624
Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met	
195 200 205	
tgg ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat	672
Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn	

210	215	220	
cac tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag			720
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys			
225	230	235	240
agt atc ttg gac tgg aca tct ttt aac cag gag aga att gtt gat gtt			768
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val			
245	250		255
gct gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac			816
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn			
260	265		270
ttt ggc ctc agc tgg aat cag caa gta act cag atg gcc ctc tgg gct			864
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala			
275	280		285
atc atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc			912
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser			
290	295		300
cct caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat			960
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn			
305	310		315
cag gac ccc ttg ggc aag caa ggg tac cag ctt aga cag gga gac aac			1008
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn			
325	330		335
ttt gaa gtg tgg gaa cga cct ctc tca ggc tta gcc tgg gct gta gct			1056
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala			
340	345		350
atg ata aac cgg cag gag att ggt gga cct cgc tct tat acc atc gca			1104
Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala			
355	360		365
gtt gct tcc ctg ggt aaa gga gtg gcc tgt aat cct gcc tgc ttc atc			1152
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile			
370	375		380
aca cag ctc ctc cct gtg aaa agg aag cta ggg ttc tat gaa tgg act			1200
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr			
385	390		395
tca agg tta aga agt cac ata aat ccc aca ggc act gtt ttg ctt cag			1248
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln			
405	410		415
cta taa			1254
Leu *			

<210> 16
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 16

Met	Gln	Leu	Arg	Asn	Pro	Glu	Leu	His	Leu	Gly	Cys	Ala	Leu	Ala	Leu
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Arg	Phe	Leu	Ala	Leu	Val	Ser	Trp	Asp	Ile	Pro	Gly	Ala	Arg	Ala	Leu
			20					25					30		
Asp	Asn	Gly	Leu	Ala	Arg	Thr	Pro	Thr	Met	Gly	Trp	Leu	His	Trp	Glu
		35					40					45			
Arg	Phe	Met	Cys	Asn	Leu	Asp	Cys	Gln	Glu	Glu	Pro	Asp	Ser	Cys	Ile
		50				55					60				
Ser	Glu	Lys	Leu	Phe	Met	Glu	Met	Ala	Glu	Leu	Met	Val	Ser	Glu	Gly
65					70					75					80
Trp	Lys	Asp	Ala	Gly	Tyr	Glu	Tyr	Leu	Cys	Ile	Asp	Asp	Cys	Trp	Met
				85					90					95	
Ala	Pro	Gln	Arg	Asp	Ser	Glu	Gly	Arg	Leu	Gln	Ala	Asp	Pro	Gln	Arg
			100					105					110		
Phe	Pro	His	Gly	Ile	Arg	Gln	Leu	Ala	Asn	Tyr	Val	His	Ser	Lys	Gly
		115					120					125			
Leu	Lys	Leu	Gly	Ile	Tyr	Ala	Asp	Val	Gly	Asn	Lys	Thr	Cys	Ala	Gly
		130				135					140				
Phe	Pro	Gly	Ser	Phe	Gly	Tyr	Tyr	Asp	Ile	Asp	Ala	Gln	Thr	Phe	Ala
145					150					155					160
Asp	Trp	Gly	Val	Asp	Leu	Leu	Lys	Phe	Asp	Gly	Cys	Tyr	Cys	Asp	Ser
				165					170					175	
Leu	Glu	Asn	Leu	Ala	Asp	Gly	Tyr	Lys	His	Met	Ser	Leu	Ala	Leu	Asn
			180					185					190		
Arg	Thr	Gly	Arg	Ser	Ile	Val	Tyr	Ser	Cys	Glu	Trp	Pro	Leu	Tyr	Met
		195					200					205			
Trp	Pro	Phe	Gln	Lys	Pro	Asn	Tyr	Thr	Glu	Ile	Arg	Gln	Tyr	Cys	Asn
		210				215						220			
His	Trp	Arg	Asn	Phe	Ala	Asp	Ile	Asp	Asp	Ser	Trp	Lys	Ser	Ile	Lys
225					230					235					240
Ser	Ile	Leu	Asp	Trp	Thr	Ser	Phe	Asn	Gln	Glu	Arg	Ile	Val	Asp	Val
			245						250					255	
Ala	Gly	Pro	Gly	Gly	Trp	Asn	Asp	Pro	Asp	Met	Leu	Val	Ile	Gly	Asn
			260					265					270		
Phe	Gly	Leu	Ser	Trp	Asn	Gln	Gln	Val	Thr	Gln	Met	Ala	Leu	Trp	Ala
		275					280					285			
Ile	Met	Ala	Ala	Pro	Leu	Phe	Met	Ser	Asn	Asp	Leu	Arg	His	Ile	Ser
		290				295					300				
Pro	Gln	Ala	Lys	Ala	Leu	Leu	Gln	Asp	Lys	Asp	Val	Ile	Ala	Ile	Asn
305					310					315					320
Gln	Asp	Pro	Leu	Gly	Lys	Gln	Gly	Tyr	Gln	Leu	Arg	Gln	Gly	Asp	Asn
			325						330					335	
Phe	Glu	Val	Trp	Glu	Arg	Pro	Leu	Ser	Gly	Leu	Ala	Trp	Ala	Val	Ala
		340						345					350		
Met	Ile	Asn	Arg	Gln	Glu	Ile	Gly	Pro	Arg	Ser	Tyr	Thr	Ile	Ala	
		355				360					365				
Val	Ala	Ser	Leu	Gly	Lys	Gly	Val	Ala	Cys	Asn	Pro	Ala	Cys	Phe	Ile

370		375		380
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr				
385		390		400
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln				
	405		410	415

Leu

<210> 17
 <211> 1272
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1272)

<400> 17	
atg cag ctg agg aac cca gaa cta cat ctg ggc tgc gcg ctt gcg ctt	48
Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu	
1 5 10 15	
cgc ttc ctg gcc ctc gtt tcc tgg gac atc cct ggg gct aga gca ctg	96
Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu	
20 25 30	
gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag	144
Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu	
35 40 45	
cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc	192
Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile	
50 55 60	
agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc	240
Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly	
65 70 75 80	
tgg aag gat gca ggt tat gag tac ctc tgc att gat gac tgt tgg atg	288
Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met	
85 90 95	
gct ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag cgc	336
Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg	
100 105 110	
ttt cct cat ggg att cgc cag cta gct aat tat gtt cac agc aaa gga	384
Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly	
115 120 125	
ctg aag cta ggg att tat gca gat gtt gga aat aaa acc tgc gca ggc	432
Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly	
130 135 140	

ttc cct ggg agt ttt gga tac tac gac att gat gcc cag acc ttt gct	480
Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala	
145 150 155 160	
gac tgg gga gta gat ctg cta aaa ttt gat ggt tgt tac tgt gac agt	528
Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser	
165 170 175	
ttg gaa aat ttg gca gat ggt tat aag cac atg tcc ttg gcc ctg aat	576
Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn	
180 185 190	
agg act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg	624
Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met	
195 200 205	
tgg ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat	672
Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn	
210 215 220	
cac tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag	720
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys	
225 230 235 240	
agt atc ttg gac tgg aca tct ttt aac cag gag aga att gtt gat gtt	768
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val	
245 250 255	
gct gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac	816
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn	
260 265 270	
ttt ggc ctc agc tgg aat cag caa gta act cag atg gcc ctc tgg gct	864
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala	
275 280 285	
atc atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc	912
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser	
290 295 300	
cct caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat	960
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn	
305 310 315 320	
cag gac ccc ttg ggc aag caa ggg tac cag ctt aga cag gga gac aac	1008
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn	
325 330 335	
ttt gaa gtg tgg gaa cga cct ctc tca ggc tta gcc tgg gct gta gct	1056
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala	
340 345 350	
atg ata aac cgg cag gag att ggt gga cct cgc tct tat acc atc gca	1104
Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala	

355	360	365	
gtt gct tcc ctg ggt aaa gga gtg gcc tgt aat cct gcc tgc ttc atc			1152
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile			
370	375	380	
aca cag ctc ctc cct gtg aaa agg aag cta ggg ttc tat gaa tgg act			1200
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr			
385	390	395	400
tca agg tta aga agt cac ata aat ccc aca ggc act gtt ttg ctt cag			1248
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln			
405	410	415	
cta tct gaa aag gac gaa tta tga			1272
Leu Ser Glu Lys Asp Glu Leu *			
420			

<210> 18
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 18

Met	Gln	Leu	Arg	Asn	Pro	Glu	Leu	His	Leu	Gly	Cys	Ala	Leu	Ala	Leu
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Arg	Phe	Leu	Ala	Leu	Val	Ser	Trp	Asp	Ile	Pro	Gly	Ala	Arg	Ala	Leu
			20					25					30		
Asp	Asn	Gly	Leu	Ala	Arg	Thr	Pro	Thr	Met	Gly	Trp	Leu	His	Trp	Glu
		35				40						45			
Arg	Phe	Met	Cys	Asn	Leu	Asp	Cys	Gln	Glu	Glu	Pro	Asp	Ser	Cys	Ile
	50				55				60						
Ser	Glu	Lys	Leu	Phe	Met	Glu	Met	Ala	Glu	Leu	Met	Val	Ser	Glu	Gly
65				70					75					80	
Trp	Lys	Asp	Ala	Gly	Tyr	Glu	Tyr	Leu	Cys	Ile	Asp	Asp	Cys	Trp	Met
			85					90					95		
Ala	Pro	Gln	Arg	Asp	Ser	Glu	Gly	Arg	Leu	Gln	Ala	Asp	Pro	Gln	Arg
			100					105					110		
Phe	Pro	His	Gly	Ile	Arg	Gln	Leu	Ala	Asn	Tyr	Val	His	Ser	Lys	Gly
			115				120					125			
Leu	Lys	Leu	Gly	Ile	Tyr	Ala	Asp	Val	Gly	Asn	Lys	Thr	Cys	Ala	Gly
	130					135					140				
Phe	Pro	Gly	Ser	Phe	Gly	Tyr	Tyr	Asp	Ile	Asp	Ala	Gln	Thr	Phe	Ala
145				150					155					160	
Asp	Trp	Gly	Val	Asp	Leu	Leu	Lys	Phe	Asp	Gly	Cys	Tyr	Cys	Asp	Ser
			165					170						175	
Leu	Glu	Asn	Leu	Ala	Asp	Gly	Tyr	Lys	His	Met	Ser	Leu	Ala	Leu	Asn
		180					185					190			
Arg	Thr	Gly	Arg	Ser	Ile	Val	Tyr	Ser	Cys	Glu	Trp	Pro	Leu	Tyr	Met
	195					200						205			
Trp	Pro	Phe	Gln	Lys	Pro	Asn	Tyr	Thr	Glu	Ile	Arg	Gln	Tyr	Cys	Asn
	210					215					220				
His	Trp	Arg	Asn	Phe	Ala	Asp	Ile	Asp	Asp	Ser	Trp	Lys	Ser	Ile	Lys

225		230		235		240									
Ser	Ile	Leu	Asp	Trp	Thr	Ser	Phe	Asn	Gln	Glu	Arg	Ile	Val	Asp	Val
			245						250					255	
Ala	Gly	Pro	Gly	Gly	Trp	Asn	Asp	Pro	Asp	Met	Leu	Val	Ile	Gly	Asn
			260					265					270		
Phe	Gly	Leu	Ser	Trp	Asn	Gln	Gln	Val	Thr	Gln	Met	Ala	Leu	Trp	Ala
			275				280					285			
Ile	Met	Ala	Ala	Pro	Leu	Phe	Met	Ser	Asn	Asp	Leu	Arg	His	Ile	Ser
			290				295				300				
Pro	Gln	Ala	Lys	Ala	Leu	Leu	Gln	Asp	Lys	Asp	Val	Ile	Ala	Ile	Asn
					310					315				320	
Gln	Asp	Pro	Leu	Gly	Lys	Gln	Gly	Tyr	Gln	Leu	Arg	Gln	Gly	Asp	Asn
				325					330					335	
Phe	Glu	Val	Trp	Glu	Arg	Pro	Leu	Ser	Gly	Leu	Ala	Trp	Ala	Val	Ala
			340					345					350		
Met	Ile	Asn	Arg	Gln	Glu	Ile	Gly	Gly	Pro	Arg	Ser	Tyr	Thr	Ile	Ala
			355				360					365			
Val	Ala	Ser	Leu	Gly	Lys	Gly	Val	Ala	Cys	Asn	Pro	Ala	Cys	Phe	Ile
			370			375					380				
Thr	Gln	Leu	Leu	Pro	Val	Lys	Arg	Lys	Leu	Gly	Phe	Tyr	Glu	Trp	Thr
					390					395				400	
Ser	Arg	Leu	Arg	Ser	His	Ile	Asn	Pro	Thr	Gly	Thr	Val	Leu	Leu	Gln
				405					410					415	
Leu	Ser	Glu	Lys	Asp	Glu	Leu									
				420											

<210> 19
 <211> 1215
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (10)...(1215)

<400> 19	
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Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg	
1 5 10	
ttc ctg gcc ctc gtt tcc tgg gac atc cct ggg gct aga gca ctg gac	99
Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp	
15 20 25 30	
aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag cgc	147
Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg	
35 40 45	
ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc agt	195
Phe Met Cys Asn Leu Asp Cys Gln Glu Pro Asp Ser Cys Ile Ser	
50 55 60	
gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc tgg	243
Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp	

65	70	75	
aag gat gca ggt tat gag tac ctc tgc att gat gac tgt tgg atg gct Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala 80 85 90			291
ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag cgc ttt Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe 95 100 105 110			339
cct cat ggg att cgc cag cta gct aat tat gtt cac agc aaa gga ctg Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu 115 120 125			387
aag cta ggg att tat gca gat gtt gga aat aaa acc tgc gca ggc ttc Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe 130 135 140			435
cct ggg agt ttt gga tac tac gac att gat gcc cag acc ttt gct gac Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp 145 150 155			483
tgg gga gta gat ctg cta aaa ttt gat ggt tgt tac tgt gac agt ttg Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser Leu 160 165 170			531
gaa aat ttg gca gat ggt tat aag cac atg tcc ttg gcc ctg aat agg Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn Arg 175 180 185 190			579
act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg tgg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met Trp 195 200 205			627
ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat cac Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn His 210 215 220			675
tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag agt Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser 225 230 235			723
atc ttg gac tgg aca tct ttt aac cag gag aga att gtt gat gtt gct Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala 240 245 250			771
gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac ttt Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe 255 260 265 270			819
ggc ctc agc tgg aat cag caa gta act cag atg gcc ctc tgg gct atc Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala Ile 275 280 285			867

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atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc cct      915
Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser Pro
      290                      295                      300

caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat cag      963
Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn Gln
      305                      310                      315

gac ccc ttg ggc aag caa ggg tac cag ctt aga cag gga gac aac ttt      1011
Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn Phe
      320                      325                      330

gaa gtg tgg gaa cga cct ctc tca ggc tta gcc tgg gct gta gct atg      1059
Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met
      335                      340                      345                      350

ata aac cgg cag gag att ggt gga cct cgc tct tat acc atc gca gtt      1107
Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val
      355                      360                      365

gct tcc ctg ggt aaa gga gtg gcc tgt aat cct gcc tgc ttc atc aca      1155
Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr
      370                      375                      380

cag ctc ctc cct gtg aaa agg aag cta ggg ttc tat gaa tgg act tca      1203
Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr Ser
      385                      390                      395

agg tta aga taa      1215
Arg Leu Arg *
      400

<210> 20
<211> 401
<212> PRT
<213> Homo sapiens

<400> 20
Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg Phe Leu
 1          5          10          15
Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp Asn Gly
 20          25          30
Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg Phe Met
 35          40          45
Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser Glu Lys
 50          55          60
Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp Lys Asp
 65          70          75          80
Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala Pro Gln
 85          90          95
Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe Pro His
100         105         110
Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu Lys Leu

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	20		25		30	
	gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag					144
	Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu					
	35		40		45	
	cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc					192
	Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile					
	50		55		60	
	agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc					240
	Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly					
	65		70		75	80
	tgg aag gat gca ggt tat gag tac ctc tgc att gat gac tgt tgg atg					288
	Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met					
		85		90		95
	gct ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag cgc					336
	Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg					
		100		105		110
	ttt cct cat ggg att cgc cag cta gct aat tat gtt cac agc aaa gga					384
	Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly					
		115		120		125
	ctg aag cta ggg att tat gca gat gtt gga aat aaa acc tgc gca ggc					432
	Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly					
		130		135		140
	ttc cct ggg agt ttt gga tac tac gac att gat gcc cag acc ttt gct					480
	Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala					
	145		150		155	160
	gac tgg gga gta gat ctg cta aaa ttt gat ggt tgt tac tgt gac agt					528
	Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser					
		165		170		175
	ttg gaa aat ttg gca gat ggt tat aag cac atg tcc ttg gcc ctg aat					576
	Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn					
		180		185		190
	agg act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg					624
	Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met					
		195		200		205
	tgg ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat					672
	Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn					
		210		215		220
	cac tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag					720
	His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys					
	225		230		235	240

		20					25			30				
Asn	Gly	Leu	Ala	Arg	Thr	Pro	Thr	Met	Gly	Trp	Leu	His	Trp	Glu
		35					40					45		Arg
Phe	Met	Cys	Asn	Leu	Asp	Cys	Gln	Glu	Glu	Pro	Asp	Ser	Cys	Ile
	50					55					60			Ser
Glu	Lys	Leu	Phe	Met	Glu	Met	Ala	Glu	Leu	Met	Val	Ser	Glu	Gly
65					70					75				80
Lys	Asp	Ala	Gly	Tyr	Glu	Tyr	Leu	Cys	Ile	Asp	Asp	Cys	Trp	Met
				85					90					95
Pro	Gln	Arg	Asp	Ser	Glu	Gly	Arg	Leu	Gln	Ala	Asp	Pro	Gln	Arg
			100					105					110	Phe
Pro	His	Gly	Ile	Arg	Gln	Leu	Ala	Asn	Tyr	Val	His	Ser	Lys	Gly
		115						120					125	Leu
Lys	Leu	Gly	Ile	Tyr	Ala	Asp	Val	Gly	Asn	Lys	Thr	Cys	Ala	Gly
	130					135					140			Phe
Pro	Gly	Ser	Phe	Gly	Tyr	Tyr	Asp	Ile	Asp	Ala	Gln	Thr	Phe	Ala
145					150				155					160
Trp	Gly	Val	Asp	Leu	Leu	Lys	Phe	Asp	Gly	Cys	Tyr	Cys	Asp	Ser
			165						170					175
Glu	Asn	Leu	Ala	Asp	Gly	Tyr	Lys	His	Met	Ser	Leu	Ala	Leu	Asn
			180					185					190	Arg
Thr	Gly	Arg	Ser	Ile	Val	Tyr	Ser	Cys	Glu	Trp	Pro	Leu	Tyr	Met
		195					200					205		Trp
Pro	Phe	Gln	Lys	Pro	Asn	Tyr	Thr	Glu	Ile	Arg	Gln	Tyr	Cys	Asn
	210				215						220			His
Trp	Arg	Asn	Phe	Ala	Asp	Ile	Asp	Asp	Ser	Trp	Lys	Ser	Ile	Lys
225					230					235				240
Ile	Leu	Asp	Trp	Thr	Ser	Phe	Asn	Gln	Glu	Arg	Ile	Val	Asp	Val
				245					250					255
Gly	Pro	Gly	Gly	Trp	Asn	Asp	Pro	Asp	Met	Leu	Val	Ile	Gly	Asn
			260					265					270	Phe
Gly	Leu	Ser	Trp	Asn	Gln	Gln	Val	Thr	Gln	Met	Ala	Leu	Trp	Ala
		275					280					285		Ile
Met	Ala	Ala	Pro	Leu	Phe	Met	Ser	Asn	Asp	Leu	Arg	His	Ile	Ser
	290					295					300			Pro
Gln	Ala	Lys	Ala	Leu	Leu	Gln	Asp	Lys	Asp	Val	Ile	Ala	Ile	Asn
305					310					315				Gln
Asp	Pro	Leu	Gly	Lys	Gln	Gly	Tyr	Gln	Leu	Arg	Gln	Gly	Asp	Asn
			325					330					335	Phe
Glu	Val	Trp	Glu	Arg	Pro	Leu	Ser	Gly	Leu	Ala	Trp	Ala	Val	Ala
			340					345					350	Met
Ile	Asn	Arg	Gln	Glu	Ile	Gly	Gly	Pro	Arg	Ser	Tyr	Thr	Ile	Ala
		355					360					365		Val
Ala	Ser	Leu	Gly	Lys	Gly	Val	Ala	Cys	Asn	Pro	Ala	Cys	Phe	Ile
	370					375					380			Thr
Gln	Leu	Leu	Pro	Val	Lys	Arg	Lys	Leu	Gly	Phe	Tyr	Glu	Trp	Thr
385				390						395				400
Arg	Leu	Arg	Ser	Glu	Lys	Asp	Glu	Leu						
				405										

<210> 23
 <211> 30
 <212> PRT
 <213> Tobacco mosaic virus

<400> 23

Thr	Ser	Arg	Leu	Arg	Ser	His	Ile	Asn	Pro	Thr	Gly	Thr	Val	Leu	Leu
1				5					10					15	
Gln	Leu	Glu	Asn	Thr	Met	Gln	Met	Ser	Leu	Lys	Asp	Leu	Leu		
			20					25					30		

<210> 24

<211> 36

<212> PRT

<213> Tobacco mosaic virus

<400> 24

Thr	Ser	Arg	Leu	Arg	Ser	His	Ile	Asn	Pro	Thr	Gly	Thr	Val	Leu	Leu
1				5					10					15	
Gln	Leu	Glu	Asn	Thr	Met	Gln	Met	Ser	Leu	Lys	Asp	Leu	Leu	Ser	Glu
			20					25					30		
Lys	Asp	Glu	Leu												
			35												

<210> 25

<211> 26

<212> PRT

<213> Tobacco mosaic virus

<400> 25

Thr	Ser	Arg	Leu	Arg	Ser	His	Ile	Asn	Pro	Thr	Gly	Thr	Val	Leu	Leu
1				5					10					15	
Gln	Leu	Glu	Asn	Thr	Met	Gln	Met	Ser	Leu						
			20					25							

<210> 26

<211> 32

<212> PRT

<213> Tobacco mosaic virus

<400> 26'

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<211> 22

<212> PRT

<213> Tobacco mosaic virus

<400> 27

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<212> DNA

<213> Tobacco mosaic virus

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Xaa Xaa Pro Xaa Ile Pro Lys Ser Phe Gly Tyr

1

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10

<210> 36

<211> 11

<212> PRT

<213> Tobacco mosaic virus

<400> 36

Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr

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<210> 37

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<212> PRT

<213> Rice

<400> 37

Ser Glu Lys Asp Glu Leu

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5